

WEST Search History

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DATE: Friday, December 17, 2004

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L16	L15 and 17	0
<input type="checkbox"/>	L15	L14 and 19	0
<input type="checkbox"/>	L14	(530/387.1,387.9,388.24,389.1,389.2)! [CCLS]	3631
<input type="checkbox"/>	L13	L12 and 111	1
<input type="checkbox"/>	L12	antibod\$.clm.	35412
<input type="checkbox"/>	L11	L10 and 17	4
<input type="checkbox"/>	L10	L9 or 18	13
<input type="checkbox"/>	L9	PARG.ab.	13
<input type="checkbox"/>	L8	PARG.ti.	8
<input type="checkbox"/>	L7	L6 or 15	3843
<input type="checkbox"/>	L6	ame.in.	995
<input type="checkbox"/>	L5	jacobson.in.	2852
<input type="checkbox"/>	L4	13 or 12 or 11	3
<input type="checkbox"/>	L3	6333148.pn.	1
<input type="checkbox"/>	L2	6337202.pn.	1
<input type="checkbox"/>	L1	6395543.pn.	1

END OF SEARCH HISTORY

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 1.32945 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-11
 Perfect score: 167
 Sequence: 1 LFTEVLHDHNECLIITGTEQYSEYTGyaETyr 31

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	167	100.0	31	3	US-09-302-812-11	Sequence 11, Appl
2	167	100.0	31	3	US-09-511-477-11	Sequence 11, Appl
3	167	100.0	31	3	US-09-511-507-11	Sequence 11, Appl
4	167	100.0	968	3	US-09-302-812-6	Sequence 6, Appli
5	167	100.0	968	3	US-09-511-477-6	Sequence 6, Appli
6	167	100.0	968	3	US-09-511-507-6	Sequence 6, Appli
7	167	100.0	976	3	US-09-302-812-4	Sequence 4, Appli
8	167	100.0	976	3	US-09-511-477-4	Sequence 4, Appli
9	167	100.0	976	3	US-09-511-507-4	Sequence 4, Appli
10	167	100.0	977	3	US-09-302-812-2	Sequence 2, Appli
11	167	100.0	977	3	US-09-511-477-2	Sequence 2, Appli

12	167	100.0	977	3	US-09-511-507-2	Sequence 2, Appli
13	82	49.1	768	3	US-09-302-812-8	Sequence 8, Appli
14	82	49.1	768	3	US-09-511-477-8	Sequence 8, Appli
15	82	49.1	768	3	US-09-511-507-8	Sequence 8, Appli
16	53.5	32.0	697	4	US-09-540-236-3601	Sequence 3601, Ap
17	53	31.7	726	3	US-09-302-812-10	Sequence 10, Appl
18	53	31.7	726	3	US-09-511-477-10	Sequence 10, Appl
19	53	31.7	726	3	US-09-511-507-10	Sequence 10, Appl
20	49.5	29.6	123	4	US-09-107-532A-5299	Sequence 5299, Ap
21	49.5	29.6	434	4	US-09-107-532A-4075	Sequence 4075, Ap
22	49	29.3	453	1	US-08-374-155A-8	Sequence 8, Appli
23	49	29.3	453	2	US-08-785-396-8	Sequence 8, Appli
24	48.5	29.0	122	4	US-09-107-532A-5851	Sequence 5851, Ap
25	48.5	29.0	330	4	US-09-540-236-3751	Sequence 3751, Ap
26	48	28.7	372	1	US-08-597-236-8	Sequence 8, Appli
27	48	28.7	372	1	US-08-746-682A-8	Sequence 8, Appli
28	48	28.7	408	4	US-09-248-796A-19266	Sequence 19266, A
29	48	28.7	993	4	US-09-894-998A-50	Sequence 50, Appl
30	48	28.7	1037	4	US-09-894-998A-54	Sequence 54, Appl
31	48	28.7	1113	4	US-09-894-998A-51	Sequence 51, Appl
32	46	27.5	230	4	US-09-328-352-7134	Sequence 7134, Ap
33	46	27.5	542	4	US-09-198-452A-1003	Sequence 1003, Ap
34	45.5	27.2	208	4	US-09-248-796A-15775	Sequence 15775, A
35	45	26.9	168	3	US-08-990-791-9	Sequence 9, Appli
36	45	26.9	168	4	US-09-372-591-9	Sequence 9, Appli
37	45	26.9	192	4	US-09-270-767-38002	Sequence 38002, A
38	45	26.9	192	4	US-09-270-767-53219	Sequence 53219, A
39	45	26.9	226	4	US-09-270-767-59161	Sequence 59161, A
40	45	26.9	342	4	US-09-543-681A-6588	Sequence 6588, Ap
41	45	26.9	371	4	US-09-270-767-43760	Sequence 43760, A
42	45	26.9	418	3	US-08-844-054-2	Sequence 2, Appli
43	45	26.9	418	3	US-09-347-333-2	Sequence 2, Appli
44	45	26.9	418	4	US-09-583-110-4220	Sequence 4220, Ap
45	45	26.9	686	2	US-08-993-228-12	Sequence 12, Appl

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 4.45213 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-11
Perfect score: 167
Sequence: 1 LFTEVLHDHNECLIITGTEQYSEYTGyaETyr 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	167	100.0	31	9	US-09-973-451-11	Sequence 11, Appl
2	167	100.0	968	9	US-09-973-451-6	Sequence 6, Appli
3	167	100.0	976	9	US-09-973-451-4	Sequence 4, Appli
4	167	100.0	977	9	US-09-973-451-2	Sequence 2, Appli
5	82	49.1	768	9	US-09-973-451-8	Sequence 8, Appli
6	72	43.1	518	17	US-10-425-115-239190	Sequence 239190,
7	72	43.1	546	15	US-10-425-114-60000	Sequence 60000, A
8	71	42.5	509	16	US-10-437-963-202306	Sequence 202306,
9	58	34.7	47	17	US-10-425-115-325463	Sequence 325463,
10	56	33.5	300	15	US-10-424-599-233915	Sequence 233915,
11	55	32.9	524	15	US-10-425-114-65345	Sequence 65345, A
12	55	32.9	529	15	US-10-425-114-65514	Sequence 65514, A
13	55	32.9	536	17	US-10-425-115-244714	Sequence 244714,
14	55	32.9	542	17	US-10-425-115-244717	Sequence 244717,
15	54.5	32.6	428	15	US-10-282-122A-52564	Sequence 52564, A
16	53	31.7	726	9	US-09-973-451-10	Sequence 10, Appl
17	52	31.1	87	17	US-10-425-115-252508	Sequence 252508,
18	52	31.1	147	16	US-10-437-963-138462	Sequence 138462,
19	50.5	30.2	86	16	US-10-437-963-150772	Sequence 150772,
20	49.5	29.6	307	15	US-10-282-122A-71975	Sequence 71975, A
21	49	29.3	224	15	US-10-425-114-45983	Sequence 45983, A
22	49	29.3	225	16	US-10-767-701-44091	Sequence 44091, A
23	49	29.3	329	15	US-10-425-114-52216	Sequence 52216, A
24	49	29.3	427	15	US-10-389-566-1764	Sequence 1764, Ap
25	49	29.3	447	15	US-10-282-122A-72107	Sequence 72107, A
26	49	29.3	453	14	US-10-061-269-8	Sequence 8, Appli
27	49	29.3	453	14	US-10-463-509-8	Sequence 8, Appli
28	49	29.3	453	14	US-10-463-569-8	Sequence 8, Appli
29	49	29.3	499	15	US-10-424-599-229000	Sequence 229000,
30	49	29.3	519	17	US-10-739-930-9479	Sequence 9479, Ap
31	49	29.3	1229	16	US-10-437-963-141907	Sequence 141907,
32	48	28.7	101	15	US-10-424-599-240498	Sequence 240498,
33	48	28.7	130	15	US-10-425-114-49850	Sequence 49850, A
34	48	28.7	413	15	US-10-389-566-1499	Sequence 1499, Ap
35	48	28.7	519	17	US-10-425-115-200991	Sequence 200991,
36	48	28.7	993	9	US-09-894-998-50	Sequence 50, Appl
37	48	28.7	993	14	US-10-121-988-50	Sequence 50, Appl
38	48	28.7	993	14	US-10-200-562-50	Sequence 50, Appl
39	48	28.7	993	14	US-10-237-551-50	Sequence 50, Appl
40	48	28.7	1037	9	US-09-894-998-54	Sequence 54, Appl
41	48	28.7	1037	14	US-10-121-988-54	Sequence 54, Appl
42	48	28.7	1037	14	US-10-200-562-54	Sequence 54, Appl
43	48	28.7	1037	14	US-10-237-551-54	Sequence 54, Appl
44	48	28.7	1113	9	US-09-894-998-51	Sequence 51, Appl
45	48	28.7	1113	14	US-10-121-988-51	Sequence 51, Appl

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 1.24368 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-12
Perfect score: 152
Sequence: 1 AYCGFLRPGVSSENLSAVATGNXGCGAFG 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	150	98.7	29	3	US-09-302-812-12	Sequence 12, Appl
2	150	98.7	29	3	US-09-511-477-12	Sequence 12, Appl
3	150	98.7	29	3	US-09-511-507-12	Sequence 12, Appl
4	149	98.0	976	3	US-09-302-812-4	Sequence 4, Appli
5	149	98.0	976	3	US-09-511-477-4	Sequence 4, Appli
6	149	98.0	976	3	US-09-511-507-4	Sequence 4, Appli
7	149	98.0	977	3	US-09-302-812-2	Sequence 2, Appli
8	149	98.0	977	3	US-09-511-477-2	Sequence 2, Appli
9	149	98.0	977	3	US-09-511-507-2	Sequence 2, Appli
10	144	94.7	968	3	US-09-302-812-6	Sequence 6, Appli
11	144	94.7	968	3	US-09-511-477-6	Sequence 6, Appli

12	144	94.7	968	3	US-09-511-507-6	Sequence 6, Appli
13	69	45.4	768	3	US-09-302-812-8	Sequence 8, Appli
14	69	45.4	768	3	US-09-511-477-8	Sequence 8, Appli
15	69	45.4	768	3	US-09-511-507-8	Sequence 8, Appli
16	60.5	39.8	543	1	US-08-375-709-17	Sequence 17, Appl
17	60.5	39.8	543	1	US-08-752-929-17	Sequence 17, Appl
18	60.5	39.8	543	3	US-09-090-793-10	Sequence 10, Appl
19	60.5	39.8	543	4	US-09-231-899-10	Sequence 10, Appl
20	53	34.9	154	4	US-09-270-767-39843	Sequence 39843, A
21	53	34.9	154	4	US-09-270-767-55060	Sequence 55060, A
22	53	34.9	403	4	US-09-170-496D-114	Sequence 114, App
23	53	34.9	403	4	US-09-170-496D-224	Sequence 224, App
24	53	34.9	403	4	US-09-743-742B-4	Sequence 4, Appli
25	53	34.9	403	4	US-09-743-742B-10	Sequence 10, Appl
26	52	34.2	708	4	US-09-248-796A-16456	Sequence 16456, A
27	50.5	33.2	411	4	US-09-540-236-3549	Sequence 3549, Ap
28	49.5	32.6	726	3	US-09-302-812-10	Sequence 10, Appl
29	49.5	32.6	726	3	US-09-511-477-10	Sequence 10, Appl
30	49.5	32.6	726	3	US-09-511-507-10	Sequence 10, Appl
31	49	32.2	1196	4	US-09-252-991A-18261	Sequence 18261, A
32	48.5	31.9	887	4	US-09-077-940A-2	Sequence 2, Appli
33	47.5	31.2	298	3	US-09-025-691-1	Sequence 1, Appli
34	46.5	30.6	134	4	US-09-621-976-4066	Sequence 4066, Ap
35	46.5	30.6	307	3	US-09-049-672A-9	Sequence 9, Appli
36	46	30.3	359	2	US-08-713-636-2	Sequence 2, Appli
37	46	30.3	681	1	US-08-083-590A-18	Sequence 18, Appl
38	46	30.3	681	2	US-08-346-128-37	Sequence 37, Appl
39	46	30.3	681	3	US-08-532-384-18	Sequence 18, Appl
40	46	30.3	1068	1	US-08-537-210A-2	Sequence 2, Appli
41	46	30.3	1068	3	US-09-113-825-2	Sequence 2, Appli
42	46	30.3	1078	1	US-08-264-534-32	Sequence 32, Appl
43	46	30.3	1078	1	US-08-083-590A-11	Sequence 11, Appl
44	46	30.3	1078	1	US-08-465-500-32	Sequence 32, Appl
45	46	30.3	1078	2	US-08-346-128-32	Sequence 32, Appl

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 4.16489 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-12
Perfect score: 152
Sequence: 1 AYCGFLRPGVSSSENLSAVATGNXGCGAFG 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	150	98.7	29	9	US-09-973-451-12	Sequence 12, Appl
2	149	98.0	976	9	US-09-973-451-4	Sequence 4, Appli
3	149	98.0	977	9	US-09-973-451-2	Sequence 2, Appli
4	144	94.7	968	9	US-09-973-451-6	Sequence 6, Appli
5	74	48.7	509	16	US-10-437-963-202306	Sequence 202306,
6	69	45.4	768	9	US-09-973-451-8	Sequence 8, Appli
7	67	44.1	518	17	US-10-425-115-239190	Sequence 239190,
8	67	44.1	546	15	US-10-425-114-60000	Sequence 60000, A
9	66	43.4	180	15	US-10-424-599-156445	Sequence 156445,
10	60.5	39.8	543	14	US-10-331-061-10	Sequence 10, Appl
11	57	37.5	104	17	US-10-425-115-239179	Sequence 239179,
12	55.5	36.5	768	14	US-10-369-493-2214	Sequence 2214, Ap
13	53	34.9	75	9	US-09-993-844-46	Sequence 46, Appl
14	53	34.9	75	15	US-10-633-438-32	Sequence 32, Appl
15	53	34.9	403	14	US-10-251-385-114	Sequence 114, App
16	53	34.9	403	14	US-10-251-385-224	Sequence 224, App
17	53	34.9	403	14	US-10-225-567A-540	Sequence 540, App
18	53	34.9	403	14	US-10-290-078-18	Sequence 18, Appl
19	53	34.9	403	14	US-10-353-690-10	Sequence 10, Appl
20	53	34.9	422	16	US-10-367-094-141	Sequence 141, App
21	53	34.9	426	15	US-10-311-671-1	Sequence 1, Appli
22	53	34.9	445	14	US-10-240-145-53	Sequence 53, Appl
23	53	34.9	445	14	US-10-240-145-139	Sequence 139, App
24	53	34.9	2762	14	US-10-123-155-13	Sequence 13, Appl
25	53	34.9	2762	14	US-10-146-731-13	Sequence 13, Appl
26	53	34.9	2762	14	US-10-140-472-13	Sequence 13, Appl
27	53	34.9	2762	14	US-10-141-761-13	Sequence 13, Appl
28	53	34.9	2762	14	US-10-142-885-13	Sequence 13, Appl
29	53	34.9	2762	14	US-10-158-790-13	Sequence 13, Appl
30	53	34.9	2762	14	US-10-137-871-13	Sequence 13, Appl
31	53	34.9	2762	14	US-10-140-923-13	Sequence 13, Appl
32	53	34.9	2762	14	US-10-141-756-13	Sequence 13, Appl
33	53	34.9	2762	14	US-10-141-759-13	Sequence 13, Appl
34	53	34.9	2762	14	US-10-140-805-13	Sequence 13, Appl
35	53	34.9	2762	14	US-10-140-864-13	Sequence 13, Appl
36	53	34.9	2762	15	US-10-142-426-13	Sequence 13, Appl
37	52	34.2	181	15	US-10-424-599-177700	Sequence 177700,
38	51	33.6	114	17	US-10-425-115-321774	Sequence 321774,
39	51	33.6	315	16	US-10-437-963-157064	Sequence 157064,
40	51	33.6	371	14	US-10-369-493-19533	Sequence 19533, A
41	51	33.6	379	9	US-09-738-626-5142	Sequence 5142, Ap
42	50.5	33.2	501	15	US-10-282-122A-63359	Sequence 63359, A
43	50	32.9	130	17	US-10-425-115-247900	Sequence 247900,
44	50	32.9	199	16	US-10-437-963-180011	Sequence 180011,
45	50	32.9	372	15	US-10-424-599-269980	Sequence 269980,

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 0.471742 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-13
 Perfect score: 53
 Sequence: 1 FLINPELIVSR 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	53	100.0	11	3	US-09-302-812-13	Sequence 13, Appl	
2	53	100.0	11	3	US-09-511-477-13	Sequence 13, Appl	
3	53	100.0	11	3	US-09-511-507-13	Sequence 13, Appl	
4	53	100.0	968	3	US-09-302-812-6	Sequence 6, Appli	
5	53	100.0	968	3	US-09-511-477-6	Sequence 6, Appli	
6	53	100.0	968	3	US-09-511-507-6	Sequence 6, Appli	
7	53	100.0	977	3	US-09-302-812-2	Sequence 2, Appli	
8	53	100.0	977	3	US-09-511-477-2	Sequence 2, Appli	
9	53	100.0	977	3	US-09-511-507-2	Sequence 2, Appli	
10	52	98.1	976	3	US-09-302-812-4	Sequence 4, Appli	
11	52	98.1	976	3	US-09-511-477-4	Sequence 4, Appli	

12	52	98.1	976	3	US-09-511-507-4	Sequence 4, Appli
13	41	77.4	252	4	US-09-198-452A-694	Sequence 694, App
14	37	69.8	1323	1	US-08-026-138E-4	Sequence 4, Appli
15	37	69.8	1336	2	US-08-231-193A-58	Sequence 58, Appl
16	37	69.8	1336	2	US-08-486-273A-58	Sequence 58, Appl
17	37	69.8	1336	3	US-08-940-086A-58	Sequence 58, Appl
18	37	69.8	1336	3	US-08-940-035A-58	Sequence 58, Appl
19	37	69.8	1336	3	US-08-935-105A-58	Sequence 58, Appl
20	37	69.8	1336	4	US-09-648-797-58	Sequence 58, Appl
21	37	69.8	1336	4	US-09-386-123-58	Sequence 58, Appl
22	36	67.9	123	4	US-09-328-352-5925	Sequence 5925, Ap
23	36	67.9	730	4	US-09-248-796A-15712	Sequence 15712, A
24	35	66.0	358	3	US-08-858-207A-398	Sequence 398, App
25	35	66.0	449	4	US-09-583-110-4686	Sequence 4686, Ap
26	34	64.2	134	4	US-09-489-039A-11592	Sequence 11592, A
27	34	64.2	409	4	US-09-540-236-2952	Sequence 2952, Ap
28	34	64.2	1065	3	US-09-412-545-2	Sequence 2, Appli
29	33	62.3	86	4	US-09-270-767-34956	Sequence 34956, A
30	33	62.3	86	4	US-09-270-767-50173	Sequence 50173, A
31	33	62.3	88	4	US-09-328-352-7192	Sequence 7192, Ap
32	33	62.3	101	4	US-09-248-796A-27320	Sequence 27320, A
33	33	62.3	176	4	US-09-107-532A-6622	Sequence 6622, Ap
34	33	62.3	313	4	US-09-551-826D-14	Sequence 14, Appl
35	33	62.3	340	4	US-09-248-796A-14931	Sequence 14931, A
36	33	62.3	400	4	US-09-543-681A-4587	Sequence 4587, Ap
37	33	62.3	452	4	US-09-198-452A-853	Sequence 853, App
38	33	62.3	556	4	US-09-248-796A-20229	Sequence 20229, A
39	33	62.3	744	4	US-09-248-796A-17602	Sequence 17602, A
40	33	62.3	883	4	US-09-489-039A-11249	Sequence 11249, A
41	32	60.4	68	4	US-09-248-796A-21149	Sequence 21149, A
42	32	60.4	68	4	US-09-248-796A-22753	Sequence 22753, A
43	32	60.4	169	2	US-08-895-939-4	Sequence 4, Appli
44	32	60.4	169	3	US-09-188-820-4	Sequence 4, Appli
45	32	60.4	169	4	US-09-617-805-7	Sequence 7, Appli

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 1.57979 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-13
Perfect score: 53
Sequence: 1 FLINPELIVSR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	11	9	US-09-973-451-13	Sequence 13, Appl
2	53	100.0	968	9	US-09-973-451-6	Sequence 6, Appli
3	53	100.0	977	9	US-09-973-451-2	Sequence 2, Appli
4	52	98.1	976	9	US-09-973-451-4	Sequence 4, Appli
5	42	79.2	119	15	US-10-424-599-168770	Sequence 168770,
6	42	79.2	509	16	US-10-437-963-202306	Sequence 202306,
7	42	79.2	518	17	US-10-425-115-239190	Sequence 239190,
8	42	79.2	546	15	US-10-425-114-60000	Sequence 60000, A
9	41	77.4	249	15	US-10-282-122A-54709	Sequence 54709, A
10	41	77.4	252	15	US-10-289-762-694	Sequence 694, App
11	38	71.7	59	15	US-10-424-599-215648	Sequence 215648,
12	37	69.8	1336	9	US-09-945-901-58	Sequence 58, Appl
13	37	69.8	1336	13	US-10-007-747-58	Sequence 58, Appl
14	37	69.8	1336	14	US-10-038-937-58	Sequence 58, Appl
15	36	67.9	107	15	US-10-424-599-183741	Sequence 183741,
16	36	67.9	473	16	US-10-437-963-124186	Sequence 124186,
17	36	67.9	519	16	US-10-437-963-124353	Sequence 124353,
18	35	66.0	449	15	US-10-282-122A-73824	Sequence 73824, A
19	35	66.0	527	14	US-10-369-493-1735	Sequence 1735, Ap
20	35	66.0	621	14	US-10-156-761-10025	Sequence 10025, A
21	35	66.0	820	14	US-10-174-677-30	Sequence 30, Appl
22	35	66.0	828	14	US-10-174-677-90	Sequence 90, Appl
23	35	66.0	932	14	US-10-174-677-89	Sequence 89, Appl
24	35	66.0	932	14	US-10-174-677-91	Sequence 91, Appl
25	34	64.2	21	15	US-10-663-896-17	Sequence 17, Appl
26	34	64.2	39	15	US-10-424-599-231144	Sequence 231144,
27	34	64.2	72	15	US-10-424-599-176489	Sequence 176489,
28	34	64.2	86	15	US-10-424-599-183835	Sequence 183835,
29	34	64.2	98	15	US-10-424-599-183834	Sequence 183834,
30	34	64.2	100	15	US-10-424-599-162739	Sequence 162739,
31	34	64.2	138	10	US-09-896-580A-8	Sequence 8, Appli
32	34	64.2	138	17	US-10-340-367-8	Sequence 8, Appli
33	34	64.2	169	10	US-09-896-580A-3	Sequence 3, Appli
34	34	64.2	169	17	US-10-340-367-3	Sequence 3, Appli
35	34	64.2	211	15	US-10-282-122A-47127	Sequence 47127, A
36	34	64.2	275	15	US-10-424-599-169986	Sequence 169986,
37	34	64.2	293	17	US-10-425-115-200086	Sequence 200086,
38	34	64.2	296	16	US-10-474-776-324	Sequence 324, App
39	34	64.2	307	15	US-10-425-114-58003	Sequence 58003, A
40	34	64.2	307	17	US-10-425-115-200087	Sequence 200087,
41	34	64.2	407	15	US-10-282-122A-63173	Sequence 63173, A
42	34	64.2	408	14	US-10-369-493-3561	Sequence 3561, Ap
43	34	64.2	449	14	US-10-369-493-20063	Sequence 20063, A
44	34	64.2	451	15	US-10-282-122A-72152	Sequence 72152, A
45	34	64.2	523	17	US-10-739-930-8452	Sequence 8452, Ap

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 0.68617 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-14
 Perfect score: 71
 Sequence: 1 IALXLPNIXTQPIPLL 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	67	94.4	16	3	US-09-302-812-14	Sequence 14, Appl
2	67	94.4	16	3	US-09-511-477-14	Sequence 14, Appl
3	67	94.4	16	3	US-09-511-507-14	Sequence 14, Appl
4	65	91.5	968	3	US-09-302-812-6	Sequence 6, Appli
5	65	91.5	968	3	US-09-511-477-6	Sequence 6, Appli
6	65	91.5	968	3	US-09-511-507-6	Sequence 6, Appli
7	65	91.5	976	3	US-09-302-812-4	Sequence 4, Appli
8	65	91.5	976	3	US-09-511-477-4	Sequence 4, Appli
9	65	91.5	976	3	US-09-511-507-4	Sequence 4, Appli
10	65	91.5	977	3	US-09-302-812-2	Sequence 2, Appli
11	65	91.5	977	3	US-09-511-477-2	Sequence 2, Appli

12	65	91.5	977	3	US-09-511-507-2	Sequence 2, Appli
13	46	64.8	768	3	US-09-302-812-8	Sequence 8, Appli
14	46	64.8	768	3	US-09-511-477-8	Sequence 8, Appli
15	46	64.8	768	3	US-09-511-507-8	Sequence 8, Appli
16	41	57.7	77	4	US-09-248-796A-24036	Sequence 24036, A
17	40	56.3	160	4	US-09-489-039A-11236	Sequence 11236, A
18	40	56.3	373	3	US-09-254-077A-12	Sequence 12, Appl
19	38	53.5	305	4	US-09-270-767-36889	Sequence 36889, A
20	38	53.5	305	4	US-09-270-767-52106	Sequence 52106, A
21	38	53.5	342	4	US-09-543-681A-5179	Sequence 5179, Ap
22	38	53.5	453	1	US-08-439-131A-5	Sequence 5, Appli
23	38	53.5	453	1	US-08-440-674-4	Sequence 4, Appli
24	38	53.5	453	4	US-08-879-337-6	Sequence 6, Appli
25	38	53.5	582	4	US-09-543-681A-4556	Sequence 4556, Ap
26	37	52.1	143	4	US-09-270-767-37600	Sequence 37600, A
27	37	52.1	143	4	US-09-270-767-52817	Sequence 52817, A
28	37	52.1	181	4	US-09-540-236-3607	Sequence 3607, Ap
29	37	52.1	341	4	US-09-489-039A-8294	Sequence 8294, Ap
30	37	52.1	366	4	US-09-540-236-3007	Sequence 3007, Ap
31	37	52.1	415	4	US-09-543-681A-6746	Sequence 6746, Ap
32	37	52.1	437	4	US-09-489-039A-12063	Sequence 12063, A
33	37	52.1	542	4	US-09-614-891-10	Sequence 10, Appl
34	37	52.1	584	4	US-09-489-039A-14137	Sequence 14137, A
35	37	52.1	597	1	US-08-399-696-102	Sequence 102, App
36	36	50.7	233	4	US-09-489-039A-12718	Sequence 12718, A
37	36	50.7	258	4	US-09-248-796A-25815	Sequence 25815, A
38	36	50.7	331	4	US-09-454-279-12	Sequence 12, Appl
39	36	50.7	341	4	US-09-543-681A-4713	Sequence 4713, Ap
40	36	50.7	445	4	US-09-252-991A-22769	Sequence 22769, A
41	36	50.7	566	4	US-09-252-991A-17972	Sequence 17972, A
42	35.5	50.0	597	4	US-09-248-796A-14379	Sequence 14379, A
43	35	49.3	101	4	US-09-345-236B-111	Sequence 111, App
44	35	49.3	172	4	US-09-270-767-32284	Sequence 32284, A
45	35	49.3	172	4	US-09-270-767-47501	Sequence 47501, A

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 2.29787 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-14
Perfect score: 71
Sequence: 1 IALXLPNIXTQPIPLL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	67	94.4	16	9	US-09-973-451-14	Sequence 14, Appl
2	65	91.5	968	9	US-09-973-451-6	Sequence 6, Appli
3	65	91.5	976	9	US-09-973-451-4	Sequence 4, Appli
4	65	91.5	977	9	US-09-973-451-2	Sequence 2, Appli
5	46	64.8	768	9	US-09-973-451-8	Sequence 8, Appli
6	43	60.6	521	14	US-10-278-173-36	Sequence 36, Appl
7	43	60.6	521	14	US-10-278-536-34	Sequence 34, Appl
8	43	60.6	521	14	US-10-225-066A-922	Sequence 922, App
9	43	60.6	521	15	US-10-374-780A-2244	Sequence 2244, Ap
10	43	60.6	521	15	US-10-412-699B-82	Sequence 82, Appl
11	41	57.7	79	15	US-10-424-599-182136	Sequence 182136,
12	41	57.7	96	17	US-10-425-115-302276	Sequence 302276,
13	41	57.7	499	14	US-10-156-761-9332	Sequence 9332, Ap
14	41	57.7	1089	14	US-10-369-493-2154	Sequence 2154, Ap
15	41	57.7	1579	9	US-09-801-368-368	Sequence 368, App
16	41	57.7	1579	14	US-10-369-493-2000	Sequence 2000, Ap
17	40	56.3	373	9	US-09-254-077A-12	Sequence 12, Appl
18	40	56.3	381	16	US-10-437-963-153754	Sequence 153754,
19	40	56.3	388	16	US-10-437-963-187460	Sequence 187460,
20	40	56.3	429	15	US-10-282-122A-58079	Sequence 58079, A
21	39	54.9	134	17	US-10-425-115-275507	Sequence 275507,
22	39	54.9	228	14	US-10-012-697-1529	GENERAL INFORMATI
23	39	54.9	1769	16	US-10-437-963-146678	Sequence 146678,
24	38	53.5	56	9	US-09-796-692-1133	Sequence 1133, Ap
25	38	53.5	56	9	US-09-796-692-1583	Sequence 1583, Ap
26	38	53.5	56	9	US-09-796-692-2200	Sequence 2200, Ap
27	38	53.5	56	14	US-10-040-862-1133	Sequence 1133, Ap
28	38	53.5	56	14	US-10-040-862-1583	Sequence 1583, Ap
29	38	53.5	56	14	US-10-040-862-2200	Sequence 2200, Ap
30	38	53.5	56	15	US-10-057-475B-1133	Sequence 1133, Ap
31	38	53.5	56	15	US-10-057-475B-1583	Sequence 1583, Ap
32	38	53.5	56	15	US-10-057-475B-2200	Sequence 2200, Ap
33	38	53.5	56	15	US-10-154-884B-1133	Sequence 1133, Ap
34	38	53.5	56	15	US-10-154-884B-1583	Sequence 1583, Ap
35	38	53.5	56	15	US-10-154-884B-2200	Sequence 2200, Ap
36	38	53.5	56	16	US-10-764-324-1133	Sequence 1133, Ap
37	38	53.5	56	16	US-10-764-324-1583	Sequence 1583, Ap
38	38	53.5	56	16	US-10-764-324-2200	Sequence 2200, Ap
39	38	53.5	91	17	US-10-425-115-199808	Sequence 199808,
40	38	53.5	91	17	US-10-425-115-295282	Sequence 295282,
41	38	53.5	329	15	US-10-282-122A-60939	Sequence 60939, A
42	38	53.5	348	9	US-09-730-617-2	Sequence 2, Appli
43	38	53.5	362	17	US-10-425-115-196937	Sequence 196937,
44	38	53.5	426	15	US-10-282-122A-61195	Sequence 61195, A
45	38	53.5	430	15	US-10-282-122A-55560	Sequence 55560, A

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 41.8993 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-2
 Perfect score: 5184
 Sequence: 1 MSAGPGCEPCTKRPRWDAAA.....YHAVESCTQTTNQPQRTGA 977

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	5184	100.0		977	3	US-09-302-812-2	Sequence 2, Appli
2	5184	100.0		977	3	US-09-511-477-2	Sequence 2, Appli
3	5184	100.0		977	3	US-09-511-507-2	Sequence 2, Appli
4	4635.5	89.4		976	3	US-09-302-812-4	Sequence 4, Appli
5	4635.5	89.4		976	3	US-09-511-477-4	Sequence 4, Appli
6	4635.5	89.4		976	3	US-09-511-507-4	Sequence 4, Appli
7	4332.5	83.6		968	3	US-09-302-812-6	Sequence 6, Appli
8	4332.5	83.6		968	3	US-09-511-477-6	Sequence 6, Appli
9	4332.5	83.6		968	3	US-09-511-507-6	Sequence 6, Appli
10	1063.5	20.5		768	3	US-09-302-812-8	Sequence 8, Appli
11	1063.5	20.5		768	3	US-09-511-477-8	Sequence 8, Appli

12	1063.5	20.5	768	3	US-09-511-507-8	Sequence 8, Appli
13	465	9.0	726	3	US-09-302-812-10	Sequence 10, Appl
14	465	9.0	726	3	US-09-511-477-10	Sequence 10, Appl
15	465	9.0	726	3	US-09-511-507-10	Sequence 10, Appl
16	167	3.2	31	3	US-09-302-812-11	Sequence 11, Appl
17	167	3.2	31	3	US-09-511-477-11	Sequence 11, Appl
18	167	3.2	31	3	US-09-511-507-11	Sequence 11, Appl
19	166	3.2	1462	4	US-09-538-092-1043	Sequence 1043, Ap
20	155.5	3.0	1804	4	US-09-362-336A-4	Sequence 4, Appli
21	153	3.0	913	3	US-08-971-089-4	Sequence 4, Appli
22	152	2.9	914	1	US-08-484-105-2	Sequence 2, Appli
23	152	2.9	914	1	US-08-484-106-2	Sequence 2, Appli
24	149.5	2.9	2224	4	US-09-054-272-38	Sequence 38, Appl
25	149	2.9	29	3	US-09-302-812-12	Sequence 12, Appl
26	149	2.9	29	3	US-09-511-477-12	Sequence 12, Appl
27	149	2.9	29	3	US-09-511-507-12	Sequence 12, Appl
28	147	2.8	26	3	US-09-302-812-19	Sequence 19, Appl
29	147	2.8	26	3	US-09-511-477-19	Sequence 19, Appl
30	147	2.8	26	3	US-09-511-507-19	Sequence 19, Appl
31	147	2.8	2004	4	US-09-538-092-1371	Sequence 1371, Ap
32	146.5	2.8	1187	1	US-08-320-559-28	Sequence 28, Appl
33	146.5	2.8	1187	3	US-08-545-860D-28	Sequence 28, Appl
34	146.5	2.8	1187	5	PCT-US94-04496-28	Sequence 28, Appl
35	146.5	2.8	1210	1	US-08-320-559-26	Sequence 26, Appl
36	146.5	2.8	1210	3	US-08-545-860D-26	Sequence 26, Appl
37	146.5	2.8	1210	4	US-09-538-092-1179	Sequence 1179, Ap
38	146.5	2.8	1210	5	PCT-US94-04496-26	Sequence 26, Appl
39	146.5	2.8	1489	4	US-09-538-092-304	Sequence 304, App
40	146	2.8	1059	4	US-09-270-767-45764	Sequence 45764, A
41	145.5	2.8	447	4	US-09-794-422-44	Sequence 44, Appl
42	144	2.8	598	4	US-09-538-092-1083	Sequence 1083, Ap
43	144	2.8	601	4	US-09-248-796A-24733	Sequence 24733, A
44	143.5	2.8	717	3	US-08-910-925-1	Sequence 1, Appli
45	143.5	2.8	1177	3	US-09-134-001C-5106	Sequence 5106, Ap

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 140.314 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-2
Perfect score: 5184
Sequence: 1 MSAGPGCEPCTKRPRWDAAA.....YHAVESCTQTTNQPQRTGA 977

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5184	100.0	977	9	US-09-973-451-2	Sequence 2, Appli
2	4635.5	89.4	976	9	US-09-973-451-4	Sequence 4, Appli
3	4332.5	83.6	968	9	US-09-973-451-6	Sequence 6, Appli
4	1063.5	20.5	768	9	US-09-973-451-8	Sequence 8, Appli
5	618	11.9	509	16	US-10-437-963-202306	Sequence 202306,
6	594	11.5	518	17	US-10-425-115-239190	Sequence 239190,
7	594	11.5	546	15	US-10-425-114-60000	Sequence 60000, A
8	465	9.0	726	9	US-09-973-451-10	Sequence 10, Appl
9	205.5	4.0	200	15	US-10-424-599-184988	Sequence 184988,
10	184	3.5	180	15	US-10-424-599-156445	Sequence 156445,
11	167	3.2	31	9	US-09-973-451-11	Sequence 11, Appl
12	166	3.2	1462	14	US-10-287-218-17	Sequence 17, Appl
13	166	3.2	1462	16	US-10-408-765A-756	Sequence 756, App
14	166	3.2	1462	16	US-10-474-291-17	Sequence 17, Appl
15	166	3.2	1462	17	US-10-473-127-1797	Sequence 1797, Ap
16	166	3.2	1462	17	US-10-473-127-1798	Sequence 1798, Ap
17	166	3.2	1462	17	US-10-473-127-1801	Sequence 1801, Ap
18	166	3.2	1462	17	US-10-473-127-1802	Sequence 1802, Ap
19	164.5	3.2	300	15	US-10-424-599-233915	Sequence 233915,
20	162.5	3.1	747	15	US-10-425-114-67803	Sequence 67803, A
21	162.5	3.1	1109	15	US-10-425-114-72939	Sequence 72939, A
22	162	3.1	748	9	US-09-864-761-43244	Sequence 43244, A
23	162	3.1	3394	16	US-10-408-765A-529	Sequence 529, App
24	161	3.1	691	15	US-10-108-260A-4345	Sequence 4345, Ap
25	160	3.1	1121	16	US-10-437-963-196036	Sequence 196036,
26	159	3.1	6642	14	US-10-369-493-5013	Sequence 5013, Ap
27	158.5	3.1	1973	15	US-10-197-824-34	Sequence 34, Appl
28	158.5	3.1	2047	15	US-10-346-863-2	Sequence 2, Appli
29	158.5	3.1	3863	15	US-10-197-824-7	Sequence 7, Appli
30	157.5	3.0	1163	14	US-10-291-172-197	Sequence 197, App
31	157.5	3.0	1163	15	US-10-221-278-197	Sequence 197, App
32	156	3.0	1235	17	US-10-416-330-39	Sequence 39, Appl
33	156	3.0	2665	9	US-09-864-761-34248	Sequence 34248, A
34	156	3.0	3664	14	US-10-177-293-423	Sequence 423, App
35	156	3.0	3664	15	US-10-263-929-143	Sequence 143, App
36	156	3.0	3664	16	US-10-408-765A-2287	Sequence 2287, Ap
37	156	3.0	3664	17	US-10-684-422-244	Sequence 244, App
38	155.5	3.0	566	15	US-10-424-599-172054	Sequence 172054,
39	155.5	3.0	1001	16	US-10-408-765A-1688	Sequence 1688, Ap
40	155.5	3.0	1501	9	US-09-924-154-17	Sequence 17, Appl
41	155.5	3.0	1804	14	US-10-275-140-2	Sequence 2, Appli
42	154	3.0	406	16	US-10-451-467A-262	Sequence 262, App
43	154	3.0	612	17	US-10-425-115-247745	Sequence 247745,
44	153	3.0	913	13	US-10-117-604-4	Sequence 4, Appli
45	152.5	2.9	460	16	US-10-767-701-42484	Sequence 42484, A

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 41.8564 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-4
 Perfect score: 5190
 Sequence: 1 MNAGPGCEPCTKATRWGAAT.....YHAVESCAETADHSGQRTGT 976

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5190	100.0	976	3	US-09-302-812-4	Sequence 4, Appli
2	5190	100.0	976	3	US-09-511-477-4	Sequence 4, Appli
3	5190	100.0	976	3	US-09-511-507-4	Sequence 4, Appli
4	4635.5	89.3	977	3	US-09-302-812-2	Sequence 2, Appli
5	4635.5	89.3	977	3	US-09-511-477-2	Sequence 2, Appli
6	4635.5	89.3	977	3	US-09-511-507-2	Sequence 2, Appli
7	4395	84.7	968	3	US-09-302-812-6	Sequence 6, Appli
8	4395	84.7	968	3	US-09-511-477-6	Sequence 6, Appli
9	4395	84.7	968	3	US-09-511-507-6	Sequence 6, Appli
10	1078	20.8	768	3	US-09-302-812-8	Sequence 8, Appli
11	1078	20.8	768	3	US-09-511-477-8	Sequence 8, Appli

12	1078	20.8	768	3	US-09-511-507-8	Sequence 8, Appli
13	463	8.9	726	3	US-09-302-812-10	Sequence 10, Appl
14	463	8.9	726	3	US-09-511-477-10	Sequence 10, Appl
15	463	8.9	726	3	US-09-511-507-10	Sequence 10, Appl
16	167	3.2	31	3	US-09-302-812-11	Sequence 11, Appl
17	167	3.2	31	3	US-09-511-477-11	Sequence 11, Appl
18	167	3.2	31	3	US-09-511-507-11	Sequence 11, Appl
19	163.5	3.2	601	4	US-09-248-796A-24733	Sequence 24733, A
20	161	3.1	2375	4	US-09-538-092-1131	Sequence 1131, Ap
21	161	3.1	2476	4	US-09-824-574-7	Sequence 7, Appli
22	159	3.1	1462	4	US-09-538-092-1043	Sequence 1043, Ap
23	154	3.0	1972	4	US-08-875-435B-3	Sequence 3, Appli
24	150.5	2.9	1177	3	US-09-134-001C-5106	Sequence 5106, Ap
25	150.5	2.9	1972	4	US-08-875-435B-4	Sequence 4, Appli
26	150	2.9	3969	3	US-08-061-376-5	Sequence 5, Appli
27	150	2.9	3969	4	US-09-538-092-1262	Sequence 1262, Ap
28	149.5	2.9	1187	1	US-08-320-559-28	Sequence 28, Appl
29	149.5	2.9	1187	3	US-08-545-860D-28	Sequence 28, Appl
30	149.5	2.9	1187	5	PCT-US94-04496-28	Sequence 28, Appl
31	149.5	2.9	1210	1	US-08-320-559-26	Sequence 26, Appl
32	149.5	2.9	1210	3	US-08-545-860D-26	Sequence 26, Appl
33	149.5	2.9	1210	4	US-09-538-092-1179	Sequence 1179, Ap
34	149.5	2.9	1210	5	PCT-US94-04496-26	Sequence 26, Appl
35	149	2.9	26	3	US-09-302-812-20	Sequence 20, Appl
36	149	2.9	26	3	US-09-511-477-20	Sequence 20, Appl
37	149	2.9	26	3	US-09-511-507-20	Sequence 20, Appl
38	149	2.9	29	3	US-09-302-812-12	Sequence 12, Appl
39	149	2.9	29	3	US-09-511-477-12	Sequence 12, Appl
40	149	2.9	29	3	US-09-511-507-12	Sequence 12, Appl
41	149	2.9	427	3	US-09-134-001C-5143	Sequence 5143, Ap
42	147	2.8	754	4	US-09-976-594-375	Sequence 375, App
43	146.5	2.8	2125	4	US-09-919-172-29	Sequence 29, Appl
44	146.5	2.8	2704	4	US-09-538-092-1260	Sequence 1260, Ap
45	144	2.8	1596	4	US-08-978-277A-4	Sequence 4, Appli

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 140.17 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-4
Perfect score: 5190
Sequence: 1 MNAGPGCEPCTKATRWGAAT.....YHAVESCAETADHSGQRTGT 976

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query		DB			ID	Description
No.	Score	Match Length					
1	5190	100.0	976	9	US-09-973-451-4	Sequence 4, Appli	
2	4635.5	89.3	977	9	US-09-973-451-2	Sequence 2, Appli	
3	4395	84.7	968	9	US-09-973-451-6	Sequence 6, Appli	
4	1078	20.8	768	9	US-09-973-451-8	Sequence 8, Appli	
5	626	12.1	509	16	US-10-437-963-202306	Sequence 202306,	
6	595	11.5	518	17	US-10-425-115-239190	Sequence 239190,	
7	595	11.5	546	15	US-10-425-114-60000	Sequence 60000, A	
8	463	8.9	726	9	US-09-973-451-10	Sequence 10, Appl	
9	217.5	4.2	200	15	US-10-424-599-184988	Sequence 184988,	
10	188	3.6	180	15	US-10-424-599-156445	Sequence 156445,	
11	179.5	3.5	300	15	US-10-424-599-233915	Sequence 233915,	
12	174	3.4	3394	16	US-10-408-765A-529	Sequence 529, App	
13	173.5	3.3	748	9	US-09-864-761-43244	Sequence 43244, A	
14	167	3.2	31	9	US-09-973-451-11	Sequence 11, Appl	
15	166.5	3.2	1163	14	US-10-291-172-197	Sequence 197, App	
16	166.5	3.2	1163	15	US-10-221-278-197	Sequence 197, App	
17	166.5	3.2	1641	16	US-10-408-765A-814	Sequence 814, App	
18	166.5	3.2	1641	16	US-10-408-765A-815	Sequence 815, App	
19	165.5	3.2	1274	15	US-10-282-122A-43837	Sequence 43837, A	
20	164.5	3.2	1111	9	US-09-815-242-12955	Sequence 12955, A	
21	161	3.1	2375	16	US-10-408-765A-277	Sequence 277, App	
22	161	3.1	2476	10	US-09-824-574-7	Sequence 7, Appli	
23	161	3.1	2492	16	US-10-697-526-2	Sequence 2, Appli	
24	159	3.1	406	16	US-10-451-467A-262	Sequence 262, App	
25	159	3.1	1462	14	US-10-287-218-17	Sequence 17, Appl	
26	159	3.1	1462	16	US-10-408-765A-756	Sequence 756, App	
27	159	3.1	1462	16	US-10-474-291-17	Sequence 17, Appl	
28	159	3.1	1462	17	US-10-473-127-1797	Sequence 1797, Ap	
29	159	3.1	1462	17	US-10-473-127-1798	Sequence 1798, Ap	
30	159	3.1	1462	17	US-10-473-127-1801	Sequence 1801, Ap	
31	159	3.1	1462	17	US-10-473-127-1802	Sequence 1802, Ap	
32	159	3.1	2419	16	US-10-408-765A-2722	Sequence 2722, Ap	
33	158.5	3.1	1948	14	US-10-032-585-7611	Sequence 7611, Ap	
34	156.5	3.0	1297	15	US-10-282-122A-71692	Sequence 71692, A	
35	155.5	3.0	1163	10	US-09-932-257A-3	Sequence 3, Appli	
36	155.5	3.0	1974	14	US-10-369-493-6395	Sequence 6395, Ap	
37	154.5	3.0	498	15	US-10-424-599-196154	Sequence 196154,	
38	154.5	3.0	3225	16	US-10-408-765A-254	Sequence 254, App	
39	153	2.9	6642	14	US-10-369-493-5013	Sequence 5013, Ap	
40	152	2.9	5176	16	US-10-437-963-150986	Sequence 150986,	
41	151	2.9	803	16	US-10-437-963-131456	Sequence 131456,	
42	151	2.9	2106	16	US-10-408-765A-2093	Sequence 2093, Ap	
43	150.5	2.9	408	15	US-10-424-599-224071	Sequence 224071,	
44	150.5	2.9	1169	15	US-10-282-122A-71179	Sequence 71179, A	
45	150.5	2.9	1312	14	US-10-369-493-1950	Sequence 1950, Ap	

OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 41.5133 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-6
 Perfect score: 5164
 Sequence: 1 MSAGPGWEPCTKARWGAAGT.....YHAVESSAETTDMPGQKAGT 968

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
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 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5164	100.0	968	3	US-09-302-812-6	Sequence 6, Appli
2	5164	100.0	968	3	US-09-511-477-6	Sequence 6, Appli
3	5164	100.0	968	3	US-09-511-507-6	Sequence 6, Appli
4	4395	85.1	976	3	US-09-302-812-4	Sequence 4, Appli
5	4395	85.1	976	3	US-09-511-477-4	Sequence 4, Appli
6	4395	85.1	976	3	US-09-511-507-4	Sequence 4, Appli
7	4332.5	83.9	977	3	US-09-302-812-2	Sequence 2, Appli
8	4332.5	83.9	977	3	US-09-511-477-2	Sequence 2, Appli
9	4332.5	83.9	977	3	US-09-511-507-2	Sequence 2, Appli
10	1074.5	20.8	768	3	US-09-302-812-8	Sequence 8, Appli
11	1074.5	20.8	768	3	US-09-511-477-8	Sequence 8, Appli

12	1074.5	20.8	768	3	US-09-511-507-8	Sequence 8, Appli
13	443.5	8.6	726	3	US-09-302-812-10	Sequence 10, Appl
14	443.5	8.6	726	3	US-09-511-477-10	Sequence 10, Appl
15	443.5	8.6	726	3	US-09-511-507-10	Sequence 10, Appl
16	167	3.2	31	3	US-09-302-812-11	Sequence 11, Appl
17	167	3.2	31	3	US-09-511-477-11	Sequence 11, Appl
18	167	3.2	31	3	US-09-511-507-11	Sequence 11, Appl
19	167	3.2	1177	3	US-09-134-001C-5106	Sequence 5106, Ap
20	163.5	3.2	1187	1	US-08-320-559-28	Sequence 28, Appl
21	163.5	3.2	1187	3	US-08-545-860D-28	Sequence 28, Appl
22	163.5	3.2	1187	5	PCT-US94-04496-28	Sequence 28, Appl
23	163.5	3.2	1210	1	US-08-320-559-26	Sequence 26, Appl
24	163.5	3.2	1210	3	US-08-545-860D-26	Sequence 26, Appl
25	163.5	3.2	1210	4	US-09-538-092-1179	Sequence 1179, Ap
26	163.5	3.2	1210	5	PCT-US94-04496-26	Sequence 26, Appl
27	159	3.1	1462	4	US-09-538-092-1043	Sequence 1043, Ap
28	153	3.0	1792	2	US-08-962-284-4	Sequence 4, Appli
29	150.5	2.9	1078	4	US-09-248-796A-20284	Sequence 20284, A
30	150	2.9	447	4	US-09-794-422-44	Sequence 44, Appl
31	150	2.9	1115	2	US-08-568-459A-2	Sequence 2, Appli
32	150	2.9	1115	2	US-08-487-826B-2	Sequence 2, Appli
33	150	2.9	1115	3	US-09-210-288-2	Sequence 2, Appli
34	150	2.9	1115	6	5198347-6	Patent No. 5198347
35	146	2.8	3924	4	US-09-538-092-1246	Sequence 1246, Ap
36	145.5	2.8	559	1	US-08-320-559-31	Sequence 31, Appl
37	145.5	2.8	559	3	US-08-545-860D-31	Sequence 31, Appl
38	145.5	2.8	559	4	US-09-538-092-1261	Sequence 1261, Ap
39	145.5	2.8	559	5	PCT-US94-04496-31	Sequence 31, Appl
40	144	2.8	26	3	US-09-302-812-21	Sequence 21, Appl
41	144	2.8	26	3	US-09-511-477-21	Sequence 21, Appl
42	144	2.8	26	3	US-09-511-507-21	Sequence 21, Appl
43	144	2.8	29	3	US-09-302-812-12	Sequence 12, Appl
44	144	2.8	29	3	US-09-511-477-12	Sequence 12, Appl
45	144	2.8	29	3	US-09-511-507-12	Sequence 12, Appl

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 139.021 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-6
Perfect score: 5164
Sequence: 1 MSAGPGWEPCTKARWGAAGT.....YHAVESSAETTDMPGQKAGT 968

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5164	100.0	968	9	US-09-973-451-6	Sequence 6, Appli
2	4395	85.1	976	9	US-09-973-451-4	Sequence 4, Appli
3	4332.5	83.9	977	9	US-09-973-451-2	Sequence 2, Appli
4	1074.5	20.8	768	9	US-09-973-451-8	Sequence 8, Appli
5	609	11.8	509	16	US-10-437-963-202306	Sequence 202306,
6	579	11.2	518	17	US-10-425-115-239190	Sequence 239190,
7	579	11.2	546	15	US-10-425-114-60000	Sequence 60000, A
8	443.5	8.6	726	9	US-09-973-451-10	Sequence 10, Appl
9	220.5	4.3	200	15	US-10-424-599-184988	Sequence 184988,
10	176	3.4	6642	14	US-10-369-493-5013	Sequence 5013, Ap
11	175	3.4	180	15	US-10-424-599-156445	Sequence 156445,
12	172.5	3.3	300	15	US-10-424-599-233915	Sequence 233915,
13	172	3.3	1489	14	US-10-115-482-18	Sequence 18, Appl
14	169.5	3.3	1297	15	US-10-282-122A-71692	Sequence 71692, A
15	167	3.2	31	9	US-09-973-451-11	Sequence 11, Appl
16	167	3.2	1169	15	US-10-282-122A-71179	Sequence 71179, A
17	165.5	3.2	787	16	US-10-473-576-23	Sequence 23, Appl
18	164.5	3.2	805	16	US-10-473-576-13	Sequence 13, Appl
19	163.5	3.2	1210	14	US-10-205-823-264	Sequence 264, App
20	161	3.1	748	9	US-09-864-761-43244	Sequence 43244, A
21	161	3.1	3394	16	US-10-408-765A-529	Sequence 529, App
22	159.5	3.1	1501	9	US-09-924-154-17	Sequence 17, Appl
23	159	3.1	1462	14	US-10-287-218-17	Sequence 17, Appl
24	159	3.1	1462	16	US-10-408-765A-756	Sequence 756, App
25	159	3.1	1462	16	US-10-474-291-17	Sequence 17, Appl
26	159	3.1	1462	17	US-10-473-127-1797	Sequence 1797, Ap
27	159	3.1	1462	17	US-10-473-127-1798	Sequence 1798, Ap
28	159	3.1	1462	17	US-10-473-127-1801	Sequence 1801, Ap
29	159	3.1	1462	17	US-10-473-127-1802	Sequence 1802, Ap
30	159	3.1	2677	14	US-10-144-194A-22	Sequence 22, Appl
31	159	3.1	2677	17	US-10-491-566-22	Sequence 22, Appl
32	159	3.1	2697	14	US-10-144-198-12	Sequence 12, Appl
33	158.5	3.1	4723	14	US-10-359-012-8	Sequence 8, Appli
34	156	3.0	691	15	US-10-108-260A-4345	Sequence 4345, Ap
35	152.5	3.0	406	16	US-10-451-467A-262	Sequence 262, App
36	152	2.9	1413	16	US-10-437-963-138262	Sequence 138262,
37	151.5	2.9	1027	16	US-10-437-963-161202	Sequence 161202,
38	150	2.9	447	10	US-09-794-422-44	Sequence 44, Appl
39	150	2.9	1115	13	US-10-153-273-2	Sequence 2, Appli
40	149.5	2.9	894	17	US-10-483-512-33	Sequence 33, Appl
41	148	2.9	1030	16	US-10-741-601-487	Sequence 487, App
42	148	2.9	1389	15	US-10-282-122A-70151	Sequence 70151, A
43	147.5	2.9	1358	14	US-10-369-493-1658	Sequence 1658, Ap
44	147.5	2.9	1973	15	US-10-197-824-34	Sequence 34, Appl
45	147.5	2.9	2047	15	US-10-346-863-2	Sequence 2, Appli